REMARKS

Claim Status

Claims 25-48 are pending, wherein claims 25, 30-33, and 39-44 are rejected, and claims 26-29, 34-38, and 45-48 are withdrawn from consideration.

To expedite the prosecution of the present application, claims 25-48 have been canceled, and claims 49-68 are newly added. Supports for the new claims are shown in the following table:

New claims	Support
49	Claim 25; page 7, 3rd paragraph
50, 62	Page 7, 4th paragraph to page 8, first two paragraphs
51	Page 7, 2nd paragraph
52, 63	Claim 30
53, 64	Claim 31
54, 65	Claim 32
55	Claim 33
56	Claim 39
57, 66	Claim 40
58, 67	Claim 43
59, 68	Claim 44
60	Claim 25; page 7, 2nd paragraph
61	page 7, 3rd paragraph

Accordingly, Applicants submit that no new matter has been added.

Rejection Under 35 U.S.C. §112, 1st Paragraph

Claims 25, 30-33 and 39-44 are rejected under 35 U.S.C. §112, 1st paragraph, for failing to comply with the written description requirement. The Examiner further states that the claims contain subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant

art that the inventor, at the time the application was filed, has possession of the claimed invention. The rejection is respectfully traversed.

Claim 49 is drawn to a method comprising the use of monotonous repeat selected from the group consisting of AT/TA, AG/CT, AAG/CTT, CGG/CCG, ATCG/CGAT, AAAT/ATTT, AAGTTC/GAACTT, CTG/CAG, TTTA/TAAA, CT/AG, and TTC/GAA (*see* page 7, 3rd paragraph). Claim 50 further limits the nucleotide sequences to one of SEQ ID NOs. 1-5 (*see* page 7, 4th paragraph to page 8, first two paragraphs). Claim 60 is drawn to a method comprising the use of monotonous repeat of two to six nucleotides, wherein the repeat has a length of about 70 to about 120 nucleotides long (*see* page 7, 2nd to 4th paragraphs).

As indicated above, all the sequences recited in the claims have been described in the specification. Moreover, as examples and illustration, the present specification shows that a sequence of 2 nucleotide-repeat (SEQ ID NO.4) was used to generate the plants shown in Figures 5 and 6; a sequence of 3 nucleotide-repeat (SEQ ID NOs.2 and 5) was used to generate the plants shown in Figures 3 and 7; a sequence of 4 nucleotide-repeat (SEQ ID NO.3) was used to generate the plants shown in Figure 4; and a sequence of 6 nucleotide-repeat (SEQ ID NO.1) was used to generate the plants shown in Figure 2.

Accordingly, Applicants submit that the subject matter of claim 49 and 60 has been clearly described in the specification in such a way as to reasonably convey to one skilled in the relevant art

that the inventor, at the time the application was filed, has possession of the claimed invention.

The Examiner contends that "it is also unclear how long the repeat will be" (page 4 of the Action, 3rd paragraph). Applicants would like to respectfully draw the Examiner's attention to page 7 of the specification, 2nd paragraph, where support may be found for the maximum length of the monotonous repeat. Accordingly, claims 51 and 60 recite the repeating sequence as between 70 and 120 nucleotides long.

The Examiner also contends that "it is unclear whether the monotonous repeats are contiguous or not" (page 5 of the Action, 4th paragraph). Applicants would like to state that it is implicitly evident in the meaning of the term "monotonous repeats" that these are contiguous repeats. The definition of "monotonous", as per the website "answers.com" is "tediously repetitious or lacking in variety", which supports the understanding that "monotonous repeats" are repeats that repeat themselves without variation, and therefore, are contiguous.

Rejection Under 35 U.S.C. §112, 1st Paragraph

Claims 25, 30-33 and 39-44 are rejected under 35 U.S.C. §112, 1st paragraph, for lack of enablement. The Examiner contends that the specification, while being enabling for a method of generating genetically diverse plants via the incorporation of one of the exogenous microsatellite sequences of SEQ ID NOs.1-5, does not reasonably provide enablement for a method of generating genetically diverse plants via the incorporation of any exogenous

microsatellite sequences. The rejection is respectfully traversed.

Claim 49 is drawn to a method comprising the use of monotonous repeat selected from the group consisting of AT/TA, AG/CT, AAG/CTT, CGG/CCG, ATCG/CGAT, AAAT/ATTT, AAGTTC/GAACTT, CTG/CAG, TTTA/TAAA, CT/AG, and TTC/GAA (*see* page 7, 3rd paragraph). Claim 50 further limits the nucleotide sequences to one of SEQ ID NOs. 1-5 (*see* page 7, 4th paragraph to page 8, first two paragraphs). The sequences recited in claim 49 include SEQ ID NOs. 1-5.

In view of the data provided on using SEQ ID NOs. 1-5 (*see* Figures 2-7) and the level of skill in the art, Applicants submit that one of ordinary skill in the art could readily practice the invention of claim 49 without undue experimentation.

Claim 60 is drawn to a method comprising the use of monotonous repeat of two to six nucleotides, wherein the repeat has a length of about 70 to about 120 nucleotides long (*see* page 7, 2nd to 4th paragraphs). As discussed above, the present specification has presented clear support to the use of monotonous repeats of two, three, four and six nucleotides (*see* Figures 2-7). It is obvious to one of ordinary skill in the art that the introduction of a monotonous repeat of five nucleotides is a clear extension of the method of the invention, and which is possible to arrive at without undue experimentation.

Applicants submit that the present application intends to provide a concept, said concept being that phenotypic variety may be generated though the insertion of micro-satellite (MS)-like

sequences. The results obtained were in fact surprising, and the invention is a proof of said concept. The number of MS-like sequences should be taken globally, i.e., five MS-like sequences displayed the same result, said result being the generation of phenotypic variability. In view of the disclosure herein and the level of skill in the art, Applicants submit that one of ordinary skill in the art could readily practice the invention of claim 60 without undue experimentation.

Rejection Under 35 U.S.C. §102

Claims 25, 30-33 and 39-44 are rejected under 35 U.S.C. 102(e) as being anticipated by Havukkala et al. (U.S. Patent Application Publication No. 2003/0018185). The Examiner contends that "Havukkala et al. teach that DNA constructs can be used to introduce microsatellite markers into transgenic plants", and that "according to the definition of microsatellite, the term refers to an array of tandemly repeated nucleotide motifs herein each motif consist of between 2 and about 10 base pairs", and that, "therefore, the reference teaches all the limitations set forth by the claims.

Applicants respectfully disagree with the Examiner. As discussed above, the present invention is drawn to methods for the generation of phenotypically diverse plants, comprising the use of monotonous repeat selected from the group consisting of AT/TA, AG/CT, AAG/CTT, CGG/CCG, ATCG/CGAT, AAAT/ATTT, AAGTTC/GAACTT, CTG/CAG, TTTA/TAAA, CT/AG, and TTC/GAA, or use of monotonous repeat of two to six nucleotides, wherein the repeat has a length of about 70 to about 120 nucleotides long.

In contrast, Havukkala et al. disclose microsatellite sequences (together with flanking sequences), and methods for their use in the detection of polymorphism. The examples of Havukkala et al. refer to (1) isolation and characterization of cDNA sequences from Eucalyptus and Pinus; and 2) PCR amplification and polymorphism analysis of Pinus DNA for detecting genetic variation. The introduction of microsatellite markers into transgenic plants is mentioned in the Discussion, for the purpose of polymorphic identification (see paragraph [0064]). No phenotypically diverse plants were generated. As a matter of fact, no plants of any kind were generated in Havukkala et al., as this publication concerned only detection. Thus, the cited publication does not teach a method for the generation of phenotypically diverse plants, and it is not enabling for the generation of phenotypically diverse plants.

Furthermore, the cited publication is restricted to the identification and isolation of microsatellite sequences obtainable from pine and eucalyptus (together with its respective, naturally occurring flanking sequences; SEQ ID NO:1-1054), and also describes three novel microsatellites (SEQ ID NO:1055-1057), based on BLASTN similarity searches, which are to be used in detection of DNA polymorphism, genome mapping, physical mapping and positional cloning of genes, variety identification, evaluation of genetic variability, fingerprinting and library screening (*see* [0033]; *see also* [0010] to [0012]).

In other words, Havukkala et al. focus on the utility of microsatellite sequences as known entities for the identification of a specific genome, species, etc. The microsatellite is viewed

as an ID number, through which a specific DNA may be identified. Havukkala et al. do not refer to microsatellite sequences as the active agents capable of generating phenotypic variability, in order to generate transgenic plants featuring various properties as presented in the present invention.

Since Havukkala et al. do not teach each and every aspect of the present invention, Havukkala et al. do not anticipate the methods of claims 49 and 60.

Rejection Under 35 U.S.C. §103(a)

Claims 25, 30-33 and 39-44 are rejected under 35 U.S.C. 103(a) as being unpatentable over Havukkala et al. (U.S. Patent Application Publication No. 2003/0018185) in view of Gallardo et al. (Planta 210:19-26 (1999)). The rejection is respectfully traversed.

Havukkala et al. has been discussed above. Gallardo et al. teach the expression of a conifer glutamine synthetase (GS) gene in transgenic poplar in order to improve nitrogen utilization efficiency in trees, wherein said transgenic poplar is generated by the insertion of an exogenous GS gene with the help of a binary vector. The Examiner contends that it would have been obvious for a person with ordinary skill in the art to clone the microsatellite sequence of Havukkala et al. into the binary vector of Gallardo et al. and further transform the resultant vector into the pine tree according to the teaching of Gallardo et al.

As mentioned above, the person with ordinary skill in the art would have no incentive, from the teachings of Havukkala, to

generate phenotypically diverse plants by cloning a microsatellite sequence in any vector, and observe its phenotypic effects on the progeny of any plant cells transformed with such construct. Havukkala et al. simply do not teach or suggest using microsatellite sequence to generate phenotypically diverse plants as claimed herein.

Hence, Applicants submit that neither the primary reference Havukkala et al., nor the combination of Havukkala and Gallardo, teach each and every aspect of the present invention. Accordingly, the present invention of claims 49 and 60 is not obvious in view of Havukkala and Gallardo.

CONCLUSION

Applicants respectfully maintain that all the grounds of rejections raised in the March 20, 2008 Office Action have been addressed and earnestly urge the Examiner to render favorable action for the claimed invention.

If a telephone interview would be of assistance in advancing prosecution of the present application, Applicants' undersigned attorney invites the Examiner to telephone him at the number provided below. If any additional fee is required, authorization is hereby given to charge the amount of any such fee to Deposit Account No. 50-1891.

Respectfully submitted,

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EXHIBIT A